

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently amended) An isolated nucleic acid molecule encoding a BEL transcription factor from *Solanum tuberosum*, wherein said isolated nucleic acid molecule:

(a) comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13; or

(b) comprises a nucleotide sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13, and that encodes a protein that comprises an amino acid sequence having a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box that are at least 90% similar to the corresponding homeodomain regions, SKY boxes, BELL domains, and VSLTLGL-boxes in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters analysis; or

(c) hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour; or

(d) encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

2. (Original) The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

3. (Currently amended) The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule comprises a nucleotide sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13, and that encodes a protein that comprises an amino acid sequence having a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box that are is at least 85-90% similar to a the corresponding homeodomain regions region, a SKY boxes box, a BELL domains domain, and a VSLTLGL-boxes box in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters analysis.

4. (Currently amended) The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under stringent high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour a hybridization buffer comprising 5X SSC at a temperature of 55°C.

5. (Original) The isolated nucleic acid molecule according to claim 1, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

6. (Original) The isolated nucleic acid molecule according to claim 2, wherein the nucleic acid molecule encodes a protein or polypeptide having a molecular mass of about 56 kDa to about 76 kDa.

7. (Original) A DNA construct comprising:
the nucleic acid molecule according to claim 1, and
an operably linked promoter and 3' regulatory region.

8. (Original) An expression vector comprising the DNA construct of claim 7.

9. (Original) The expression vector according to claim 8, wherein the nucleic acid molecule is in proper sense orientation and correct reading frame.

10. (Original) A host cell transduced with the nucleic acid molecule according to claim 1.

11. (Currently amended) The host cell according to claim 10, wherein the cell is selected from the group consisting of a bacterial cell, a virus, a yeast cell, an insect cell, a plant cell, and [[a]] an isolated mammalian cell.

12. (Original) A transgenic plant transformed with the nucleic acid molecule according to claim 1.

13. (Original) The transgenic plant according to claim 12, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

14. (Currently amended) The transgenic plant according to claim 12, wherein the nucleic acid molecule comprises a nucleotide sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13, and that encodes a protein that comprises an amino acid sequence having a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box that are at least 85-90% similar to a the corresponding homeodomain regions region, a SKY boxes box, a BELL domains domain, and a VSLTLGL-boxes box in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters analysis.

15. (Currently amended) The transgenic plant according to claim 12, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under stringent high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour a hybridization buffer comprising 5X SSC at a temperature of 55°C.

16. (Original) The transgenic plant according to claim 12, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

17. (Original) The transgenic plant according to claim 12, wherein the nucleic acid molecule encodes a protein or polypeptide having a molecular mass of about 56 kDa to about 76 kDa.

18. (Original) The transgenic plant according to claim 12, wherein the plant is selected from the group consisting of Gramineae, Liliaceae, Iridaceae, Orchidaceae, Salicaceae, Ranunculaceae, Magnoliaceae, Cruciferae, Rosaceae, Leguminosae, Malvaceae, Umbelliferae, Labiate, Solanaceae, Cucurbitaceae, Compositae, and Rubiaceae.

19. (Original) A transgenic plant seed transformed with the nucleic acid molecule according to claim 1.

20. (Original) The transgenic plant seed according to claim 19, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

21. (Currently amended) The transgenic plant seed according to claim 19, wherein the nucleic acid molecule comprises a nucleotide sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID

NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13,
and that encodes a protein that comprises an amino acid sequence having a homeodomain
region, a SKY box, a BELL domain, and a VSLTLGL-box that are at least 85 90% similar
to a the corresponding homeodomain regions region, a SKY boxes box, a BELL domains
domain, and a VSLTLGL-boxes box in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6,
SEQ ID NO:8, SEQ ID NO:10.

22. (Currently amended) The transgenic plant seed according to claim 19, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under stringent high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour a hybridization buffer comprising 5X SSC at a temperature of 55°C.

23. (Original) The transgenic plant seed according to claim 19, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

24. (Original) The transgenic plant seed according to claim 19, wherein the nucleic acid molecule encodes a protein or polypeptide having a molecular mass of about 56 kDa to about 76 kDa.

25. (Original) The transgenic plant seed according to claim 19, wherein the plant seed is selected from the group consisting of Gramineae, Liliaceae, Iridaceae, Orchidaceae, Salicaceae, Ranunculaceae, Magnoliaceae, Cruciferae, Rosaceae, Leguminosae, Malvaceae, Umbelliferae, Labiate, Solanaceae, Cucurbitaceae, Compositae, and Rubiaceae.

Claims 26-42 (canceled)

43. (Currently amended) A method for enhancing growth in increasing rate of growth of a plant comprising:

transforming a plant with a the DNA construct according to claim 7 comprising:

a nucleic acid molecule encoding a BEL transcription factor from Solanum tuberosum, and

an operably linked promoter and 3' regulatory region, whereby the rate of growth in of the plant is increased enhanced.

44. (Original) The method according to claim 43, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

45. (Currently amended) The method according to claim 43, wherein the nucleic acid molecule comprises a nucleotide sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13, and that encodes a protein that comprises an amino acid sequence having a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box that are is at least 85 90% similar to a the corresponding homeodomain regions region, a SKY boxes box, a BELL domains domain, and a VSLTLGL-boxes box in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters.

46. (Currently amended) The method according to claim 43, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under stringent high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour a hybridization buffer comprising 5X SSC at a temperature of 55°C.

47. (Original) The method according to claim 43, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

48. (Currently amended) The method according to claim 43, wherein the first nucleic acid molecule encodes a protein or polypeptide having a molecular mass of about 56 kDa to about 76 kDa.

49. (Original) The method according to claim 43, wherein the plant is selected from the group consisting of Gramineae, Liliaceae, Iridaceae, Orchidaceae, Salicaceae, Ranunculaceae, Magnoliaceae, Cruciferae, Rosaceae, Leguminosae, Malvaceae, Umbelliferae, Labiate, Solanaceae, Cucurbitaceae, Compositae, and Rubiaceae.

50. (Currently amended) A method for regulating flowering in a plant comprising:

transforming a plant with a the DNA construct according to claim 7
~~comprising:~~

~~a nucleic acid molecule encoding a BEL transcription factor from
Solanum tuberosum, and~~

~~an operably linked promoter and 3' regulatory region, whereby
flowering in the plant is regulated.~~

51. (Original) The method according to claim 50, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

52. (Currently amended) The method according to claim 50, wherein the nucleic acid molecule comprises a nucleic acid sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13, and that encodes a protein that comprises an amino acid sequence having a homeodomain region, a

SKY box, a BELL domain, and a VSLTLGL-box that are is at least 85-90% similar to a the corresponding homeodomain regions region, a SKY boxes box, a BELL domains domain, and a VSLTLGL-boxes box in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters analysis.

53. (Currently amended) The method according to claim 50, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under stringent high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour a hybridization buffer comprising 5X SSC at a temperature of 55°C.

54. (Original) The method according to claim 50, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

55. (Currently amended) The method according to claim 50, wherein the first nucleic acid molecule encodes a protein or polypeptide having a molecular mass of about 56 kDa to about 76 kDa.

56. (Original) The method according to claim 50, wherein the plant is selected from the group consisting of Gramineae, Liliaceae, Iridaceae, Orchidaceae, Salicaceae, Ranunculaceae, Magnoliaceae, Cruciferae, Rosaceae, Leguminosae, Malvaceae, Umbelliferae, Labiate, Solanaceae, Cucurbitaceae, Compositae, and Rubiaceae.

57. (New) The DNA construct according to claim 7, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

58. (New) The DNA construct according to claim 7, wherein the nucleic acid molecule comprises a nucleotide sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13, and that encodes a protein that comprises an amino acid sequence having a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box that are at least 90% similar to the corresponding homeodomain regions, SKY boxes, BELL domains, and VSLTLGL-boxes in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters.

59. (New) The DNA construct according to claim 7, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour.

60. (New) The DNA construct according to claim 7, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

61. (New) The expression vector according to claim 8, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

62. (New) The expression vector according to claim 8, wherein the nucleic acid molecule comprises a nucleotide sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13, and that encodes a protein that comprises an amino acid sequence having a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box that are at least 90% similar to the

corresponding homeodomain regions, SKY boxes, BELL domains, and VSLTLGL-boxes in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters.

63. (New) The expression vector according to claim 8, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour.

64. (New) The expression vector according to claim 8, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.

65. (New) The host cell according to claim 10, wherein the nucleic acid molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

66. (New) The host cell according to claim 10, wherein the nucleic acid molecule comprises a nucleotide sequence that is at least 90% similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, and SEQ ID NO:13, and that encodes a protein that comprises an amino acid sequence having a homeodomain region, a SKY box, a BELL domain, and a VSLTLGL-box that are at least 90% similar to the corresponding homeodomain regions, SKY boxes, BELL domains, and VSLTLGL-boxes in either SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14 by basic BLAST using default parameters.

67. (New) The host cell according to claim 10, wherein the nucleic acid molecule hybridizes to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or SEQ ID NO:13 under high stringency conditions characterized by hybridization in a buffer of 4-5X SSC/0.1% w/v SDS at 54°C for 1-3 hours and in 4X SSC at 65°C, followed by a washing in 0.1X SSC at 65°C for about one hour.

68. (New) The host cell according to claim 10, wherein the nucleic acid molecule encodes a protein or polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, and SEQ ID NO:14.